

**ASSESSING STRIPE RUST (*Puccinia striiformis* f. sp. *tritici*)
POPULATION STRUCTURE USING MOLECULAR METHODS**

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Yellow rust caused by the fungus *Puccinia striiformis* f. sp. *tritici* (Pst), may induce severe yield losses under favorable conditions. It is considered one of the most important pathogens of wheat. The risk of the decreasing quantity of yield depends on the frequency and speed of spreading of new fungus races. Knowledge of the pathogen population structure is one of the key elements of resistance breeding and sustainable agriculture.

In this study 48 single uredinium Pst isolates obtained from wheat, triticale and rye from six localizations in Poland in year 2022 were assessed. DNA from Pst isolates was extracted using CTAB method. Assessment of the isolates was carried out using two methods: analysis of SSR profiles for 19 loci (Ali et al. 2011) and MARPLE (Mobile And Real-time PLant disEase; Radhakrishnan et al. 2019).

The SSR method can be easily implemented in most laboratories using existing equipment and is a robust tool used to characterize isolate races. MARPLE allowed us to obtain much more data and information about the isolates, however it takes up more resources, both in consumable reagents as well as computing power and data disc storage.

The *P. striiformis* population in Poland was diverse. Both methods allow us for rapid identification of known races or new variants. Monitoring of the pathogen population and knowledge of its genetic structure is very important for crop protection and resistance breeding.

Keywords: MARPLE, SSR, yellow rust, pathogen